

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 15:33:20 ; Search time 47 seconds

(without alignments)

51.013 Million cell updates/sec

Title: US-10-600-389a-3

Perfect score: 145

Sequence: 1 MKSFITRKNPAILATVAATGAIAGAYYY 29

Scoring table: BLOCKSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_5/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score

Query Match Length

DB ID

Description

Sequence 3, Appli

Sequence 27, Appli

Sequence 37, Appli

Sequence 26, Appli

Sequence 28, Appli

Sequence 27, Appli

Sequence 29, Appli

Sequence 40, Appli

Sequence 40, Appli

Sequence 36, Appli

Sequence 41, Appli

Sequence 89, Appli

Sequence 31, Appli

Sequence 74, Appli

Sequence 17, Appli

Sequence 23, Appli

Sequence 32, Appli

Sequence 25, Appli

Sequence 14, Appli

Sequence 14, Appli

Sequence 17246, Appli

Sequence 772, Appli

28	51	35.2	835	2	US-09-438-185A-728
29	50.5	34.8	739	2	US-09-503-922-1
30	50	34.5	140	2	US-09-530-914A-9
31	50	34.5	602	2	US-09-569-037-6
32	49	33.8	201	2	US-09-605-703B-488
33	49	33.8	238	2	US-09-605-703B-486
34	49	33.8	348	2	US-09-931-401B-2
35	49	33.8	501	2	US-09-530-851-2
36	49	33.8	777	2	US-09-543-681A-4272
37	48	33.1	230	2	US-09-134-00C-4631
38	48	33.1	244	2	US-09-252-991A-22373
39	48	33.1	507	2	US-09-949-016-11300
40	48	33.1	977	2	US-08-335-844A-22
41	48	33.1	977	2	US-09-129-366-22
42	47	32.4	140	2	US-09-252-991A-21038
43	47	32.4	198	2	US-09-107-532A-6808
44	47	32.4	275	2	US-09-107-532A-7236
45	47	32.4	345	2	US-09-328-352-6565

ALIGNMENTS

RESULT 1
US-10-165-873D-3
; Sequence 3 , Application US/10165873D

GENERAL INFORMATION:

; APPLICANT: Peng, Gang
; APPLICANT: Hopper, James E.
; APPLICANT: Vyshkina, Tamara E.
; TITLE OF INVENTION: Reagents And Methods For Detection And Characterization Of Protein-Protein Interactions, Nuclear Export And Localization Of Sequences And Inducible Gal4P-Mediated Gene Expression In Yeast

; TITLE OF INVENTION: Sequences And Inducible Gal4P-Mediated Gene Expression In Yeast

; FILE REFERENCE: 02-133

; CURRENT APPLICATION NUMBER: US/10/165-873D

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: 60/296383

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 3

; LENGTH: 29

; TYPE: PRT

; ORGANISM: Artificial sequence.

; FEATURE: OTHER INFORMATION: mitochondria outer membrane signal anchor

US-10-165-873D-3

Query Match Score 145; DB 2; Length 29;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKSFITRKNPAILATVAATGAIAGAYYY 29
Db 1 MKSFITRKNPAILATVAATGAIAGAYYY 29

RESULT 2
US-08-789-333F-27
; Sequence 27, Application US/08789333F

; APPLICANT: Rothenberg, S. M.
; Patent No. 6153380

; GENERAL INFORMATION:

; APPLICANT: No. 6153380an, Garry P

US/08789333F

; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR EFFECTOR PEPTIDES AND RNA MOLECULES

; TITLE OF INVENTION: A642601D1BRMSDSS

; CURRENT APPLICATION NUMBER: US/08/789-333F

; CURRENT FILING DATE: 1997-01-23

; PRIOR APPLICATION NUMBER: 08/589,108

; PRIOR FILING DATE: 1996-01-23

; PRIOR APPLICATION NUMBER: 08/589,911

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OM protein - protein search, using sw model

Run on: March 16, 2006, 15:36:21 ; Search time 195 Seconds

(without alignments)
36.052 Million cell updates/sec

Title: US-10-600-389A-1.
Perfect score: 86

Scoring table: BLOSUM62
Sequence: 1 MGCTVSTQQTGDBSDP 16

Searched: 2443163 seqs, 419378781 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_21:*

1: geneseq19908:*

2: geneseq19908:*

3: geneseq20008:*

4: geneseq20016:*

5: geneseq20025:*

6: geneseq2003ab:*

7: geneseq2003bb:*

8: geneseq20048:*

9: geneseq20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	86	100.0	16	6	ABP97556	Abp97556 Amino aci	
2	86	100.0	16	6	ABP97553	Abp97553 N-myristoyl	
3	86	100.0	16	8	ADH51063	Adh51063 Myristoyl	
4	86	100.0	17	6	ABP97558	Abp97558 Amino aci	
5	86	100.0	66	2	AAW69646	AAw69646 N-termina	
6	86	100.0	66	2	AAW69646	AAw69646 N-termina	
7	86	100.0	66	2	AAW69644	AAw69644 N-termina	
8	86	100.0	66	2	AAW69644	AAw69644 N-termina	
9	86	100.0	66	2	AAW69645	AAw69645 N-termina	
10	86	100.0	66	2	AAW74443	AAw74443 Human Gal	
11	86	100.0	66	2	AAW74442	AAw74442 Human Gal	
12	86	100.0	66	2	AAW74440	AAw74440 Human Gal	
13	86	100.0	66	2	AAW74445	AAw74445 Human Gal	
14	86	100.0	66	2	AAW74441	AAw74441 Human Gal	
15	86	100.0	66	2	AB20745	Ab20745 GPA1 amin	
16	86	100.0	66	3	AB20750	Ab20750 GPA1 and	
17	86	100.0	66	3	AB20750	Ab20750 GPA1 and	
18	86	100.0	66	3	AB20751	Ab20751 GPA1 and	
19	86	100.0	66	3	AB20753	Ab20753 GPA1 and	
20	86	100.0	66	6	ABU10277	Abu10277 N-termina	
21	86	100.0	66	6	ABU10284	Abu10284 N-termina	
22	86	100.0	66	6	ABU10285	Abu10285 N-termina	
23	86	100.0	66	6	ABU10282	Abu10282 N-termina	
24	86	100.0	66	6	ABU10282	Abu10282 N-termina	

25	86	100.0	66	8	ADI37116	Yeast cel	
26	86	100.0	66	8	ADI37118	Yeast cel	
27	86	100.0	66	8	ADI37115	Yeast cel	
	28	86	100.0	66	8	ADI37117	Yeast cel
	29	86	100.0	66	8	ADI37110	Yeast cel
	30	86	100.0	66	8	ADSI5955	Yeast GPA
	31	86	100.0	66	8	ADSI5961	Yeast GPA
	32	86	100.0	66	8	ADSI5963	Yeast GPA
	33	86	100.0	66	8	ADSI5960	Yeast GPA
	34	86	100.0	66	8	ADSI5962	Yeast GPA
	35	86	100.0	472	2	AAV02220	Chimeric
	36	86	100.0	472	2	AAV02222	Chimeric
	37	86	100.0	472	2	AAV02224	Chimeric
	38	86	100.0	472	2	AAV02217	Chimeric
	39	86	100.0	472	2	AAV02225	Chimeric
	40	86	100.0	472	2	AAV02218	Chimeric
	41	86	100.0	472	2	AAV02223	Chimeric
	42	86	100.0	472	2	AAV02219	Chimeric
	43	86	100.0	472	2	AAV02221	Chimeric
	44	86	100.0	472	8	AD643591	Bacterial
	45	86	100.0	892	2	AAW16314	Human thr
	46	86	100.0	906	2	AAW16313	Yeast alp
	47	80	93.0	16	6	ABP57554	Variant N
	48	80	93.0	16	8	ADH51064	Myristoyl
	49	71	82.6	478	2	AAV02226	Putative
	50	49	57.0	457	8	ADX66746	Plant ful
	51	48	55.8	1887	6	ABU20638	Protein e
	52	44	51.2	99	2	AAV49558	Sequence
	53	44	51.2	267	8	ADY70883	Plant ful
	54	43	50.0	280	6	ABU45571	Protein e
	55	43	50.0	315	8	ADN7747	Thermoc
	56	42	48.8	27	5	AAU9413	Insulin/i
	57	42	48.8	250	6	ABU48134	Protein e
	58	42	48.8	296	8	ADX3313	Plant ful
	59	42	48.8	314	4	AAB396250	Putative
	60	42	48.8	314	6	ABU29263	Protein e
	61	42	48.8	314	8	AD513182	Bacterial
	62	42	48.8	314	8	ADN18637	Bacterial
	63	42	48.8	314	8	ADSA1926	Enteroc
	64	42	48.8	317	7	ADH88571	Enteroc
	65	42	48.8	409	6	ABU11446	Protein e
	66	42	48.8	458	4	AAU36166	Klebsiell
	67	42	48.8	458	6	ABU31195	Protein e
	68	42	48.8	474	7	ABO64180	Klebsiell
	69	42	48.8	594	8	ADY25234	Plant ful
	70	42	48.8	826	8	ADH71222	Human pro
	71	42	48.8	826	8	ADH71270	Human pro
	72	42	48.8	826	8	ADH71276	Human pro
	73	42	48.8	826	8	ADH71260	Human pro
	74	42	48.8	826	8	ADH71278	Human pro
	75	42	48.8	826	8	ADH71280	Human pro
	76	42	48.8	832	8	ADH71224	Human pro
	77	42	48.8	2144	8	ADQ19484	Human sof
	78	42	48.8	2333	8	ADH71274	Human pro
	79	42	48.8	2733	4	AAU05680	FCT
	80	42	48.8	2733	7	ADB32024	Human FCT
	81	42	48.8	2733	8	ADH71250	Human pro
	82	42	48.8	2733	8	ADH71254	Human pro
	83	42	48.8	2733	8	ADH71240	Human pro
	84	42	48.8	2733	8	ADH71246	Human pro
	85	42	48.8	2733	8	ADH71258	Human pro
	86	42	48.8	2802	5	ADH71253	Chicken N
	87	42	48.8	2733	8	ABH97264	Novel hum
	88	41.5	48.3	413	5	ABG18865	Cyclin d
	89	41	47.7	27	5	AAU89437	Insulin/i
	90	41	47.7	79	4	Aau53330	Propionib
	91	41	47.7	79	6	ABM49849	Propionib
	92	41	47.7	146	6	ABO27187	Human sig
	93	41	47.7	201	4	ABG18865	Novel hum
	94	41	47.7	211	8	ADx87734	Plant ful
	95	41	47.7	314	4	Aau35229	Enteroc
	96	41	47.7	361	2	AAR42281	PGE2 rece
	97	41	47.7	365	2	AAR42280	PGE2 rece